Listing of Claims:

This Listing of Claims will replace all prior versions, and listings, of claims in the application.

1-38. (Canceled)

39. (Previously presented) A method for the detection of tumors associated with the generation of at least one uPAR deletion variant comprising the steps of:

(a) obtaining a cDNA containing sample from a tumor to be investigated, and

(b) analyzing the cDNA of said sample to determine whether alternative splicing of uPAR has occurred and at least one uPAR deletion variant has been generated, wherein the at least one uPAR deletion variant is del5 or del4+5, wherein the tumor sample is obtained from a human patient,

wherein the presence of at least one uPAR deletion variant in said tumor indicates the presence of a tumor associated with the generation of at least one uPAR deletion variant.

40. (Previously presented) The method according to claim 39, wherein the step of analyzing the cDNA of said sample comprises: amplifying the cDNA to obtain a quantified control amplification product comprising the nucleic acid coding for wild type uPAR and a quantified amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant, and determining the ratio of wild type uPAR:uPAR deletion variant by comparing the quantified amplification products.

41. (Previously presented) The method according to claim 39, wherein the cDNA is amplified with a first set of primers complementary to sequences contained in regions bridging the deleted sequences in uPAR deletion variants to obtain the amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant, and wherein the cDNA is amplified with a second set of primers complementary to sequences contained in the wild type uPAR to obtain the control amplification product comprising the nucleic acid coding for wild type uPAR.

42. (Previously presented) The method according to claim 39, wherein the amplification of the cDNA is done by real-time RT-PCR amplification.

43-44. Canceled.

45. (Previously presented) The method according to claim 39, wherein the method provides a prognosis for tumors associated with the generation of at least one uPAR deletion variant.

46. (Previously presented) The method according to claim 40, wherein the ratio of wild type uPAR:uPAR deletion variant is greater than 0.043.

47. (Previously presented) The method according to claim 45, wherein the tumors are selected from the group consisting of breast, ovarian, small cell lung, and pancreatic tumors.

48. (Previously presented) The method according to claim 45, wherein the tumor is breast tumor.

49. (Previously presented) The method according to claim 45, wherein the prognosis comprises characterization of the tumors, said characterization comprising indicating whether the tumors are more invasive, are more likely to have metastasis, are more likely to have a shorter disease free survival period or are more likely to have higher rates of recurrence than tumors not associated with the generation of uPAR deletion variants.

50-55. (Canceled)

56. (Previously presented) A method of providing a prognosis for a tumor-bearing patient comprising the steps of:

(a) obtaining a cDNA containing sample from a tumor of said patient,

(b) analyzing the cDNA of said sample to determine whether alternative splicing of uPAR has occurred and at least one uPAR deletion variant has been generated, wherein the at least one uPAR deletion variant is del5 or del4+5, and

(c) correlating the presence of the at least one uPAR deletion variant in the tumor of the patient with a prognosis of the patient.

57. (Previously presented) The method according to claim 56, wherein the step of analyzing the cDNA of said sample comprises: amplifying the cDNA to obtain a quantified control amplification product comprising the nucleic acid coding for wild type uPAR and a quantified amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant, and determining the ratio of wild type uPAR:uPAR deletion variant by comparing the quantified amplification products.

58. (Previously presented) The method according to claim 56, wherein the cDNA is amplified with a first set of primers complementary to sequences contained in regions bridging the deleted sequences in uPAR deletion variants to obtain the amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant, and wherein the cDNA is amplified with a second set of primers complementary to sequences contained in the wild type uPAR to obtain the control amplification product comprising the nucleic acid coding for wild type uPAR.

59. (Previously presented) The method according to claim 56, wherein the amplification of the cDNA is done by real-time RT-PCR amplification.

60. Canceled.

61. (Previously presented) The method according to claim 56, wherein the tumor is a breast, ovarian, small cell lung, or pancreatic tumor.